



SEQUENCE LISTING

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<120> PLANT NUCLEOTIDE SUGAR PYROPHOSPHATASE/PHOSPHODIESTERASE (NPPASE), METHOD OF PRODUCTION, USE IN THE MANUFACTURE OF TESTING DEVICES AND IN THE PRODUCTION OF TRANSGENIC PLANTS

<130> U015575-8

<140> 10/520696
<141> 2005-01-06

<150> PCT/ES03/000363
<151> 2003-07-15

<160> 24

<170> PatentIn version 3.3

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<212> PRT
<213> HORDEUM VULGARE CV. SCARLETT

<220>
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<223> N-terminal end of soluble NPPase

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Ala Ala Val Arg Ala Ser Pro Asp Leu Leu Gly Ser Arg Gly Glu
1 5 10 15

<210> 2
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<223> Tryptic sequence of soluble NPPase

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<222> (6)..(6)

PPV
<223> Xaa can be Gln or Lys

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<222> (9)..(9)

<223> Xaa can be Leu or Ile

<220>

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<222> (10)..(10)

<223> Xaa can be Lys or Gln

<400> 2

Ala Ser Tyr Pro Gly Xaa Thr Ser Xaa Xaa Arg
1 5 10

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<223> Tryptic sequence of soluble NPPase

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<223> Xaa can be Met or Phe

<400> 3

His Ala Pro Ala Asp Thr Val Thr Xaa Gly Arg
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<210> 4

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<212> PRT

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<223> Tryptic sequence of soluble NPPase

<400> 4

Ala Pro Pro Tyr Pro
1 5

<210> 5
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<223> Tryptic sequence of soluble NPPase

<400> 5

Ala Trp Val Thr Val Glu Phe Lys
1 5

<210> 6
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<223> Tryptic sequence of soluble NPPase

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<220>
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<223> Xaa can be Ile or Leu

<220>
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<223> Xaa can be Ile or Leu

<400> 6

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1 5

<210> 7
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<213> ORYZA SATIVA

<220>

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<223> N-terminal end of soluble NPPase

<400> 7

Gly Ser Ala Phe Val Ser Ala Thr Pro Ala Leu Leu Gly Asp Gln
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<210> 8
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<213> ORYZA SATIVA

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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 8

Phe Gln Leu Leu Asn Gln Arg Tyr Asp Phe Ser Phe Ala Leu Glu Thr
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Gly Gly Leu Glu Asn Pro Lys
20

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<213> ORYZA SATIVA

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<223> Tryptic sequence (MS/MS) of soluble NPPase

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Leu Val Ala Val Ser Glu Ala Leu Ser Phe Lys
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<400> 10

Leu Ala Gln Gly Lys Ser Tyr Asp Glu Met
1 5 10

<210> 11

<211> 10

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<213> ORYZA SATIVA

<220>

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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 11

Thr Ala Ala Gly Thr Leu Thr Phe Asn Arg
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<210> 12

<211> 11

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<213> ORYZA SATIVA

<220>

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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 12

Asp Pro Gly Phe Leu His Thr Ala Phe Leu Arg
1 5 10

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<213> ORYZA SATIVA

<220>

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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 13

Ala Pro Asp Phe Pro Gly Gln Asn Ser Leu Gln Arg
1 5 10

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<213> ORYZA SATIVA

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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 14

Ile Ile Val Phe Gly Asp Met Gly Lys
1 5

<210> 15
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<220>
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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 15

Asp Trp Pro Asn Thr Gly Gly Phe Phe Asp Val Lys
1 5 10

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<223> Tryptic sequence (MS/MS) of soluble NPPase

<400> 16

Phe Ile Glu Gln Cys Leu Ser Thr Val Asp Arg
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<400> 17

Val Tyr Asp Ser Phe Tyr Val Glu Arg
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<210> 18
<211> 18
<212> DNA
<213> ORYZA SATIVA

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<223> Primer of the 5' region of NPPase

<400> 18
ggcgttgctc ggcgacca 18

<210> 19
<211> 19
<212> DNA
<213> ORYZA SATIVA

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<223> Primer of the 3' region of NPPase

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<212> DNA
<213> ORYZA SATIVA

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<221> misc_feature
<223> complete cDNA of rice NPPase

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tcgctgaaag gttccagcc gctgtcgaag atcggcgccac acaaggccac cgtcgacctc 180

cacggctccg cgttcgtag cgccacgccg gcgttgctcg gcgaccaggg agaagacaca 240
gagtgggtca cggtaaaata cggctggca aacccttccg ctgacgactg gattgctgtc 300
ttctctccgg ccgatttcat ctcgggttct tgccctaata cttccagata cccggatgag 360
ccgctgctct gcactgcacc aataaagtat caattcgcaa actactcgac gaactacgtg 420
tactggggca agggcagcat ccggttccag ctcataacc agcgctacga ctctcccttc 480
gccctgttca ccggccgcct ggaaaaccct aagctggtgg cgggtcgaa ggcgatatcg 540
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gagtgatcg 2040
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<223> Amino acid sequence of rice NPPase

<400> 21

Met Val Ser Arg Lys Arg Gly Gly Gly Gly Val Ala Met Ala Val
1 5 10 15

Ala Met Leu Leu Ala Ala Ser Ala Ser Arg Pro Ser Ser Ser Leu
20 25 30

Glu Gly Phe Gln Pro Leu Ser Lys Ile Ala Val His Lys Ala Thr Val
35 40 45

Asp Leu His Gly Ser Ala Phe Val Ser Ala Thr Pro Ala Leu Leu Gly
50 55 60

Asp Gln Gly Glu Asp Thr Glu Trp Val Thr Val Lys Tyr Gly Trp Ala
65 70 75 80

Asn Pro Ser Ala Asp Asp Trp Ile Ala Val Phe Ser Pro Ala Asp Phe
85 90 95

Ile Ser Gly Ser Cys Pro Asn Pro Ser Arg Tyr Pro Asp Glu Pro Leu
100 105 110

Leu Cys Thr Ala Pro Ile Lys Tyr Gln Phe Ala Asn Tyr Ser Ala Asn
115 120 125

Tyr Val Tyr Trp Gly Lys Gly Ser Ile Arg Phe Gln Leu Ile Asn Gln
130 135 140

Arg Tyr Asp Phe Ser Phe Ala Leu Phe Thr Gly Gly Leu Glu Asn Pro
145 150 155 160

Lys Leu Val Ala Val Ser Glu Ala Ile Ser Phe Lys Asn Pro Lys Ala
165 170 175

Pro Val Tyr Pro Arg Leu Ala Gln Gly Lys Ser Tyr Asp Glu Met Thr
180 185 190

Val Thr Trp Thr Ser Gly Tyr Asp Ile Ser Glu Ala Tyr Pro Phe Val
195 200 205

Glu Trp Gly Met Val Val Ala Gly Ala Ala Ala Pro Thr Arg Thr Ala
210 215 220

Ala Gly Thr Leu Thr Phe Asn Arg Gly Ser Met Cys Gly Asp Pro Asp
225 230 235 240

Arg Thr Val Gly Trp Arg Asp Pro Gly Phe Ile His Thr Ala Phe Leu
245 250 255

Arg Asp Leu Trp Pro Asn Lys Glu Tyr Tyr Tyr Lys Ile Gly His Glu
260 265 270

Leu Ser Asp Gly Ser Ile Val Trp Gly Lys Gln Tyr Thr Phe Arg Ala
275 280 285

Pro Pro Phe Pro Gly Gln Asn Ser Leu Gln Arg Ile Ile Val Phe Gly
290 295 300

Asp Met Gly Lys Ala Glu Arg Asp Gly Ser Asn Glu Phe Ala Asn Tyr
305 310 315 320

Gln Pro Gly Ser Leu Asn Thr Thr Asp Arg Leu Val Glu Asp Leu Asp
325 330 335

Asn Tyr Asp Ile Val Phe His Ile Gly Asp Leu Pro Tyr Ala Asn Gly
340 345 350

Tyr Ile Ser Gln Trp Asp Gln Phe Thr Ala Gln Val Ala Pro Ile Thr
355 360 365

Ala Lys Lys Pro Tyr Met Ile Ala Ser Gly Asn His Glu Arg Asp Trp
370 375 380

Pro Asn Thr Gly Gly Phe Phe Asp Val Lys Asp Ser Gly Gly Glu Cys
385 390 395 400

Gly Val Pro Ala Glu Thr Met Tyr Tyr Pro Ala Glu Asn Arg Ala
405 410 415

Asn Phe Trp Tyr Lys Val Asp Tyr Gly Met Phe Arg Phe Cys Ile Ala
420 425 430

Asp Ser Glu His Asp Trp Arg Glu Gly Thr Asp Gln Tyr Lys Phe Ile
435 440 445

Glu Gln Cys Leu Ser Thr Val Asp Arg Lys His Gln Pro Trp Leu Ile
450 455 460

Phe Ala Ala His Arg Val Leu Gly Tyr Ser Ser Asn Trp Trp Tyr Ala
465 470 475 480

Asp Gln Gln Ser Phe Glu Glu Pro Glu Gly Arg Glu Ser Leu Gln Arg
485 490 495

Leu Trp Gln Arg His Arg Val Asp Val Ala Phe Phe Gly His Val His
500 505 510

Asn Tyr Glu Arg Thr Cys Pro Met Tyr Gln Ser Gln Cys Val Ser Gly
515 520 525

Glu Arg Arg Arg Tyr Ser Gly Thr Met Asn Gly Thr Ile Phe Val Val
530 535 540

Ala Gly Gly Gly Ser His Leu Ser Asp Tyr Thr Ser Ala Ile Pro

545

550

555

560

Lys Trp Ser Val Phe Arg Asp Arg Asp Phe Gly Phe Val Lys Leu Thr
565 570 575

Ala Phe Asn His Ser Ser Leu Leu Phe Glu Tyr Lys Lys Ser Ser Asp
580 585 590

Gly Lys Val Tyr Asp Ser Phe Thr Val Glu Arg Asp Tyr Arg Asp Val
595 600 605

Leu Ser Cys Val His Asp Ser Cys Leu Pro Thr Thr Leu Ala Ser
610 615 620

<210> 22

<211> 1268

<212> DNA

<213> HORDEUM VULGARE CV. SCARLETT

<220>

<221> misc_feature

<223> Incomplete cDNA of barley NPPase

<400> 22

ctccgacgga agcgtggtgt gggccaagcc ctacacttcc cgggcaccgc caaccccccgg 60

gcagaactcg ctgcagcgta tcatcgctt cggtgacatg ggaaaggcgg agagggacgg 120

atcaaacgag ttcgccaact accagccggg gtcgctcaac acgacggaca ggctgattga 180

agatctggac aactacgaca tcgtcttcca catcgccgac atgccctacg ccaacgggta 240

cctctcccag tgggaccagt tcaccgcaca ggtcgccccc atcagcgcca agaaacccta 300

catggttgca agcggcaacc acgagagggc ctggcccaac accggcgggt tcttcgacgt 360

caaggactcc ggcggcgaat gcggcgtgcc ggccgagacc atgtactact accccgcccga 420

aaacagggca aacttctggc acaagggtgga ctacggatg ttccgggtct gcgtggggga 480

ctcggagcac gactggaggg agggcacccc gcagtacaag ttcatcgagg agtgcctgtc 540

gacggtggac cggaagcacc agccgtggct catcttcacg ggcgcaccggg tgctgggcta 600

ctcctccaac tcgtggtagc ccgaccaggg ctccttcagag gagcccgagg gacgggagag 660

cctgcagaag ctgtggcagc gtcaccgcgt cgacatcgcc tccttcggcc acgtccacaa 720

ctacgagcgc acatgcccgc tctaccagag ccagtgcgtc aacgcccaca agaccacta 780
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caagctcacc gcattcaacc actcctcgct tctcttcgag tacatgaaga gcagcgacgg 960
caaggctcac gactccttca ccatccacag ggattaccgc gacgtgctca gctgcgtgca 1020
cgacagctgc ttccccacca cgctcgctag ctagctcata tcgtccggcc gtcatgtcaa 1080
tgtaatggag ggtcatccat ccaataaaat tgtgggcatg tggtagttaaaaattgg 1140
cagctgcaca atttatatgt gctagtaaaa agatcatgca agaggtgggt gtatgctcg 1200
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<211> 350
<212> PRT
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<220>
<221> misc_feature
<223> Amino acid sequence deduced from the cDNA of barley NPPase
<400> 23

Ser Asp Gly Ser Val Val Trp Ala Lys Pro Tyr Thr Phe Arg Ala Pro
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Pro Thr Pro Gly Gln Asn Ser Leu Gln Arg Ile Ile Val Phe Gly Asp
20 25 30

Met Gly Lys Ala Glu Arg Asp Gly Ser Asn Glu Phe Ala Asn Tyr Gln
35 40 45

Pro Gly Ser Leu Asn Thr Thr Asp Arg Leu Ile Glu Asp Leu Asp Asn
50 55 60

Tyr Asp Ile Val Phe His Ile Gly Asp Met Pro Tyr Ala Asn Gly Tyr
65 70 75 80

Leu Ser Gln Trp Asp Gln Phe Thr Ala Gln Val Ala Pro Ile Ser Ala

85

90

95

Lys Lys Pro Tyr Met Val Ala Ser Gly Asn His Glu Arg Asp Trp Pro
100 105 110

Asn Thr Gly Gly Phe Phe Asp Val Lys Asp Ser Gly Gly Glu Cys Gly
115 120 125

Val Pro Ala Glu Thr Met Tyr Tyr Tyr Pro Ala Glu Asn Arg Ala Asn
130 135 140

Phe Trp Tyr Lys Val Asp Tyr Gly Met Phe Arg Phe Cys Val Gly Asp
145 150 155 160

Ser Glu His Asp Trp Arg Glu Gly Thr Pro Gln Tyr Lys Phe Ile Glu
165 170 175

Glu Cys Leu Ser Thr Val Asp Arg Lys His Gln Pro Trp Leu Ile Phe
180 185 190

Thr Ala His Arg Val Leu Gly Tyr Ser Ser Asn Ser Trp Tyr Ala Asp
195 200 205

Gln Gly Ser Phe Glu Glu Pro Glu Gly Arg Glu Ser Leu Gln Lys Leu
210 215 220

Trp Gln Arg Tyr Arg Val Asp Ile Ala Ser Phe Gly His Val His Asn
225 230 235 240

Tyr Glu Arg Thr Cys Pro Leu Tyr Gln Ser Gln Cys Val Asn Ala Asp
245 250 255

Lys Thr His Tyr Ser Gly Thr Met Asn Gly Thr Ile Phe Val Val Ala
260 265 270

Gly Gly Gly Ser His Leu Ser Ser Tyr Thr Thr Ala Ile Pro Lys
275 280 285

Trp Ser Ile Phe Arg Asp His Asp Tyr Gly Phe Thr Lys Leu Thr Ala
290 295 300

Phe Asn His Ser Ser Leu Leu Phe Glu Tyr Met Lys Ser Ser Asp Gly
305 310 315 320

Lys Val Tyr Asp Ser Phe Thr Ile His Arg Asp Tyr Arg Asp Val Leu
325 330 335

Ser Cys Val His Asp Ser Cys Phe Pro Thr Thr Leu Ala Ser
340 345 350

<210> 24
<211> 39
<212> DNA
<213> HORDEUM VULGARE CV. SCARLETT

<220>
<221> misc_feature
<223> Primer of the 5' region of NPPase

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39